Jarrell, Noble

From:

Ramirez, Delia

Sent:

Wednesday, April 19, 2006 6:24 PM

To: Subject:

Jarrell, Noble 10/665455

Hi,

I would like to request the following alignments: SEQ ID NO:1 against SEQ ID NO:2-7.

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

SHEW 4(13/06 YEN TO 1967 SPA SUM FNA

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Results of SIM with:

Sequence 2: UserSeq2, (177 residues) Sequence 1: UserSeq1, (180 residues)

using the parameters

Number of alignments computed: 20 Comparison matrix: BLOSUM62

Gap extension penalty: 4 Gap open penalty: 12

SER ID NO:1 15 SERIDNO:2

(PROTEIN) TRANSCATION)



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH

UserSeq2, UserSeq1, 98.9% identity in 177 residues overlap; Score: 927.0; Gap frequency: 0.0% MPIKYKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLØF\$AMASFRREMVNTLGIER MPIEYKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLL@SSAMASFRREMVNTLGIER

1

http://us.expasy.org/cgi-bin/sim.pl?prot

```
UserSeq1,
UserSeq2,
UserSeq2,
                   UserSeq1,
                                                                                                                                                                                  UserSeq1,
                                                                                                                                                                                                                                                                                                                            UserSeq2
                                                                                                                                                            UserSeq2,
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                                                                    26.7% identity in
                                                                                                                                                                                                                                                                                                                                                  UserSeq1,
                                                                                                                                                                                                                                                                                                                                                                                                57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%
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                                                                                                                                                                                                                                                                                                                              136
                       154 GYACAYSSAFMGREI
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GYQSGLKDAELARKI
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                                                                 residues overlap; Score: 21.0; Gap frequency: 0.0%
                                                                                                                                                                                                                               residues overlap; Score: 21.0; Gap frequency: 0.0%
```

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Results of SIM with:

Sequence 2: UserSeq2, (180 residues) Sequence 1: UserSeq1, (180 residues)

using the parameters

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4

SENID NO:1 US SERID NO:3



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

UserSeq1, 98.3% identity in 180 residues overlap; Score: 941.0; Gap frequency: 0.0%

MP ήΘΎ KPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQ \$\$AMASFRREMVNTLGIER

UserSeq2,

MP İKYKPE I QHSDFKDLTNLI HFQSMEGKI WLGEQRMLLLQF SAMASFRREMVNTLGI ER ********************************

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UserSeq2,
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                    UserSeq1,
                                                                           33.3% identity in
                                                                                                                                                                                                  UserSeq1,
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  107 KVRPTGLDI
                                                                                                                                                                            154 GYACAYSSAFMGREI
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                         KLRPNASEV
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                                                                         residues overlap; Score: 21.0; Gap frequency: 0.0%
                                                                                                                                                                                                                                                       residues overlap; Score: 21.0; Gap frequency: 0.0%
```

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Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

SEN ID NO: 1 VS SEDIDNO: 4

using the parameters

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

UserSeq1, 97.8% identity in 180 residues overlap; Score: 938.0; Gap frequency: 0.0% MPIEKKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQSSAMASFRREMVNTLGIER

MP 1K K K PE 1R HSDF KDLTNLIHF QSMEGKI WLGEQRMLLLQF SAMASFRREMVNTLGIER 0

UserSeq2,



```
UserSeq2,
                                               UserSeq1,
                                                                                                                                       UserSeq2,
                                                                                                                                                                 UserSeq1,
                                                    121
                     121 RFYAEMEWIDWFEVEICQTDLGQMQDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGCGG
                                                                                                                                          61
                                                 RFYAEMEWIDWFEVEICQTDLGQMQDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGCGG
                                                                                                                                     AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDMEYG
                                                                                                                                                                AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDΙ Φ̈́Κ̀ΈΥG
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```

```
UserSeq1,
UserSeq2,
                                                                  36.4% identity in 11 residues overlap; Score: 24.0; Gap frequency: 0.0%
  107
 KVRPTELDIDM
                       KLRPNASEVGM
```

```
UserSeq2,
                     UserSeq1,
                                                                    57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%
 148 VCWTVLG
                       136 ICQTDLG
```

```
57.1% identity in
       7
residues overlap; Score: 22.0; Gap frequency: 0.0%
```

```
UserSeq2,
       UserSeq1,
136
        148
ICQTDLG
        VCWTVLG
```

^{26.7%} identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq2,	UserSeq1,
154 GYACAYSSAFMGREI	69 GYQSGLKDAELARKL

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Results of SIM with:

Sequence 2: UserSeq2, (180 residues) Sequence 1: UserSeq1, (180 residues)

using the parameters

SECONDIDIONELLS SECONDIDIOS

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.2% identity in 180 residues overlap; Score: 936.0; Gap frequency: 0.0%

UserSeq2, UserSeq1,

MPI/EΥKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLØS\$AMASFRREMVNTLG/ΓΈR

بر بر MP¶KYKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQF\$AMASFRREMVNTLGVER \************************ ************

42

```
UserSeq1,
UserSeq2,
UserSeq2,
                    UserSeq1,
                                                                  26.7% identity in
                                                                                                                                                                         UserSeq1,
                                                                                                                                                                                                                                                                                                          UserSeq2
                                                                                                                                                                                                                                                                                                                               UserSeq1,
                                                                                                                                                    UserSeq2,
                                                                                                                                                                                                                                                                                                                                                                          57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UserSeq2,
                                                                                                                                                                                                                       26.7% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UserSeq1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UserSeq2,
                      154 GYACAYSSAFMGREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148
                                                                                                                                                     154 GYACAYSSAFMGREI
                                                                                                                                                                                                                                                                                                           136 ICQTDLG
                                                                                                                                                                                                                                                                                                                                 148 VCWTVLG
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 69 GYQSGLKDAELARKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                            GYQSGLKDAELARKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |TKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDKEYG
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                                                                 residues overlap; Score: 21.0;
                                                                                                                                                                                                                      residues overlap;
                                                                                                                                                                                                                        Score:
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                                                                                                                                                                                                                       21.0;
                                                               Gap frequency: 0.0%
                                                                                                                                                                                                                     Gap frequency: 0.0%
```

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Results of SIM with:

Sequence 2: UserSeq2, (180 residues) Sequence 1: UserSeq1, (180 residues)

using the parameters

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4

SEO DIOS SOLDIOS



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.2% identity in 180 residues overlap; Score: 932.0; Gap frequency: 0.0%

MP¶KŸKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLL@F\$AMASFRREMVNTLGIER MPIÆYKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQS\$AMASFRREMVNTLGIER ************ ***********

UserSeq2, UserSeq1,

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40.0% identity in
                                                                                                                     UserSeq2,
                                                                                                                                              UserSeq1,
                                                                                                                                                                                                                                            UserSeq2,
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                                                                                                                   121 RFYAEMEWIDWFEVEICQTDLGQMQDPVCWTVLGYACAYSSALMGREIIFKEVSCRGCGG
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                                                                                                                                                   RFYAEMEWIDWFEVEICQTDLGQMQDPVCWTVLGYACAYSSAFWGREIIFKEVSCRGCGG
                                                                                                                                                                                                                                              AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIGREYG
                                                                                                                                                                                                                                                                         AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDI|DK|EYG
                                                                                            *****************
10 residues overlap; Score: 26.0; Gap frequency: 0.0%
```

UserSeq1, UserSeq2, 107 82 KVRPTELDIG KLRPNASEVG

UserSeq2, UserSeq1, 57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0% 136 ICQTDLG 148 VCWTVLG

identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 136 ICQTDLG
UserSeq2, 148 VCWTVLG
* * * **

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 154 GYACAYSSAFMGREI
UserSeq2, 69 GYQSGLKDAELARKL



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You can also have a look at a sample screen of LALNVIEW and access its documentation. Click here to download LALNVIEW (Unix, Mac and PC versions available).

Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

SER 10 20:1 10 SER (2 XD:7

using the parameters

Number of alignments computed: 20 Comparison matrix: BLOSUM62

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

98.3% identity in 180 residues overlap; Score: 941.0; Gap frequency: 0.0%

UserSeq2, UserSeq1,

ΜΡ ΓΙΈΥ KPEI QHSDFKDLTNLIHFQSMEGKIWLGEQRMLLL Θ΄SSAMASFRREMVNTLGIER

MP¶KYKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQF\$AMASFRREMVNTLGIER ************

75



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UserSeq1,
UserSeq2,
UserSeq2,
                  UserSeq1,
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                                                               33.3% identity in
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  KLRPNASEV
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                                                             9 residues overlap; Score:
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                                                                                                                                                                                                                                                                                                                                                         residues overlap; Score: 21.0; Gap frequency: 0.0%
                                                                                                                                                                                                             residues overlap;
                                                                                                                                                                                                           Score:
                                                          20.0; Gap frequency: 0.0%
                                                                                                                                                                                                           21.0; Gap frequency: 0.0%
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